

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/572,976
Source: JFWP
Date Processed by STIC: 04/10/2006

ENTERED

IFWP

RAW SEQUENCE LISTING

DATE: 04/10/2006

PATENT APPLICATION: US/10/572,976

TIME: 10:44:52

Input Set : F:\6550-086POA SeqListing.ST25.txt

Output Set: N:\CRF4\04102006\J572976.raw

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3 <110> APPLICANT: Board of Trustees operating Michigan State University
4      Frost, John W.
6 <120> TITLE OF INVENTION: Methods and Materials for the Production of Shikimic Acid
8 <130> FILE REFERENCE: 6550-000086
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/572,976
C--> 10 <141> CURRENT FILING DATE: 2006-03-22
10 <150> PRIOR APPLICATION NUMBER: US 60/505,658
11 <151> PRIOR FILING DATE: 2003-09-24
13 <160> NUMBER OF SEQ ID NOS: 34
15 <170> SOFTWARE: PatentIn version 3.3
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 618
19 <212> TYPE: DNA
20 <213> ORGANISM: Escherichia coli
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (1)..(615)
26 <223> OTHER INFORMATION: dgoA CDS for KDPGal Aldolase
28 <400> SEQUENCE: 1
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30 Met Gln Trp Gln Thr Lys Leu Pro Leu Ile Ala Ile Leu Arg Gly Ile
31 1          5          10          15
33 acg ccc gac gag gcg ctg gcg cat gtt ggc gcg gtg att gac gcc ggg      96
34 Thr Pro Asp Glu Ala Leu Ala His Val Gly Ala Val Ile Asp Ala Gly
35          20          25          30
37 ttc gac gcg gtt gaa atc ccg ctg aat tcc cca caa tgg gag caa agc      144
38 Phe Asp Ala Val Glu Ile Pro Leu Asn Ser Pro Gln Trp Glu Gln Ser
39          35          40          45
41 att ccc gcc atc gtt gat gcg tac ggc gac aag gcg ttg att ggc gca      192
42 Ile Pro Ala Ile Val Asp Ala Tyr Gly Asp Lys Ala Leu Ile Gly Ala
43          50          55          60
45 ggt acg gta ctg aaa cct gaa cag gtc gat gcg ctc gcc agg atg ggc      240
46 Gly Thr Val Leu Lys Pro Glu Gln Val Asp Ala Leu Ala Arg Met Gly
47 65          70          75          80
49 tgt cag ctc atc gtt acg ccc aat atc cat agt gaa gtg atc cgc cgt      288
50 Cys Gln Leu Ile Val Thr Pro Asn Ile His Ser Glu Val Ile Arg Arg
51          85          90          95
53 gcg gtg ggc tac ggc atg acc gtc tgc ccc ggc tgc gcg acg gcg acc      336
54 Ala Val Gly Tyr Gly Met Thr Val Cys Pro Gly Cys Ala Thr Ala Thr
55          100          105          110
57 gaa gcc ttt acc gcg ctc gaa gcg ggc gcg cag gcg ctg aaa ata ttt      384
58 Glu Ala Phe Thr Ala Leu Glu Ala Gly Ala Gln Ala Leu Lys Ile Phe
59          115          120          125

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61 ccg tca tcg gct ttt ggt ccg caa tac atc aaa gcg tta aaa gcg gta      432
62 Pro Ser Ser Ala Phe Gly Pro Gln Tyr Ile Lys Ala Leu Lys Ala Val
63      130      135      140
65 ttg cca tcg gac atc gca gtc ttt gcc gtt ggc ggc gtg acg cca gaa      480
66 Leu Pro Ser Asp Ile Ala Val Phe Ala Val Gly Gly Val Thr Pro Glu
67 145      150      155      160
69 aac ctg gcg cag tgg ata gac gca ggt tgt gca ggg gcg ggc tta ggc      528
70 Asn Leu Ala Gln Trp Ile Asp Ala Gly Cys Ala Gly Ala Gly Leu Gly
71      165      170      175
73 agc gat ctc tat cgc gcc ggg caa tcc gta gag cgc acc gcg cag cag      576
74 Ser Asp Leu Tyr Arg Ala Gly Gln Ser Val Glu Arg Thr Ala Gln Gln
75      180      185      190
77 gca gca gca ttt gtt aag gcg tat cga gag gca gtg caa tga      618
78 Ala Ala Ala Phe Val Lys Ala Tyr Arg Glu Ala Val Gln
79      195      200      205
82 <210> SEQ ID NO: 2
83 <211> LENGTH: 205
84 <212> TYPE: PRT
85 <213> ORGANISM: Escherichia coli
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90 1      5      10      15
93 Thr Pro Asp Glu Ala Leu Ala His Val Gly Ala Val Ile Asp Ala Gly
94      20      25      30
97 Phe Asp Ala Val Glu Ile Pro Leu Asn Ser Pro Gln Trp Glu Gln Ser
98      35      40      45
101 Ile Pro Ala Ile Val Asp Ala Tyr Gly Asp Lys Ala Leu Ile Gly Ala
102      50      55      60
105 Gly Thr Val Leu Lys Pro Glu Gln Val Asp Ala Leu Ala Arg Met Gly
106 65      70      75      80
109 Cys Gln Leu Ile Val Thr Pro Asn Ile His Ser Glu Val Ile Arg Arg
110      85      90      95
113 Ala Val Gly Tyr Gly Met Thr Val Cys Pro Gly Cys Ala Thr Ala Thr
114      100      105      110
117 Glu Ala Phe Thr Ala Leu Glu Ala Gly Ala Gln Ala Leu Lys Ile Phe
118      115      120      125
121 Pro Ser Ser Ala Phe Gly Pro Gln Tyr Ile Lys Ala Leu Lys Ala Val
122      130      135      140
125 Leu Pro Ser Asp Ile Ala Val Phe Ala Val Gly Gly Val Thr Pro Glu
126 145      150      155      160
129 Asn Leu Ala Gln Trp Ile Asp Ala Gly Cys Ala Gly Ala Gly Leu Gly
130      165      170      175
133 Ser Asp Leu Tyr Arg Ala Gly Gln Ser Val Glu Arg Thr Ala Gln Gln
134      180      185      190
137 Ala Ala Ala Phe Val Lys Ala Tyr Arg Glu Ala Val Gln
138      195      200      205
141 <210> SEQ ID NO: 3
142 <211> LENGTH: 618
143 <212> TYPE: DNA

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Input Set : F:\6550-086POA SeqListing.ST25.txt

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144 <213> ORGANISM: Klebsiella pneumoniae
147 <220> FEATURE:
148 <221> NAME/KEY: CDS
149 <222> LOCATION: (1)..(615)
150 <223> OTHER INFORMATION: dgoA CDS for KDPGal Aldolase
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154 Met Gln Trp Gln Thr Asn Leu Pro Leu Ile Ala Ile Leu Arg Gly Ile
155 1          5          10          15
157 acg cca gac gag gcg ctg gct cac gtt ggc gcc gtt atc gac gcc ggt      96
158 Thr Pro Asp Glu Ala Leu Ala His Val Gly Ala Val Ile Asp Ala Gly
159          20          25          30
161 ttc gac gcg gtc gaa atc ccg ctg aac tcg ccg cag tgg gag aaa agt      144
162 Phe Asp Ala Val Glu Ile Pro Leu Asn Ser Pro Gln Trp Glu Lys Ser
163          35          40          45
165 att ccg cag gtc gtc gac gct tac ggc gag cag gcg ctt atc ggc gcg      192
166 Ile Pro Gln Val Val Asp Ala Tyr Gly Glu Gln Ala Leu Ile Gly Ala
167          50          55          60
169 ggc acg gtg ctg caa ccg gag cag gtc gac agg ctg gcg gcc atg ggc      240
170 Gly Thr Val Leu Gln Pro Glu Gln Val Asp Arg Leu Ala Ala Met Gly
171 65          70          75          80
173 tgt cgg ctg att gtg acg cca aac att caa ccg gaa gtg atc cgg cga      288
174 Cys Arg Leu Ile Val Thr Pro Asn Ile Gln Pro Glu Val Ile Arg Arg
175          85          90          95
177 gcg gtg ggt tac ggc atg acc gtg tgt cca ggc tgc gcc acc gcc agc      336
178 Ala Val Gly Tyr Gly Met Thr Val Cys Pro Gly Cys Ala Thr Ala Ser
179          100          105          110
181 gaa gcc ttt agc gcg ctc gat gcc ggc gcg cag gcg cta aaa atc ttc      384
182 Glu Ala Phe Ser Ala Leu Asp Ala Gly Ala Gln Ala Leu Lys Ile Phe
183          115          120          125
185 ccg tca tcg gct ttt ggc ccg gat tac atc aaa gcg ttg aaa gcc gtg      432
186 Pro Ser Ser Ala Phe Gly Pro Asp Tyr Ile Lys Ala Leu Lys Ala Val
187          130          135          140
189 ctg ccg ccc gag gtt ccg gtc ttt gcc gtt ggc ggc gtg acg ccg gaa      480
190 Leu Pro Pro Glu Val Pro Val Phe Ala Val Gly Gly Val Thr Pro Glu
191 145          150          155          160
193 aac ctg gcg cag tgg att aat gcc ggc tgt gtt ggg gca gga ttg ggt      528
194 Asn Leu Ala Gln Trp Ile Asn Ala Gly Cys Val Gly Ala Gly Leu Gly
195          165          170          175
197 agc gat ctc tat cgt gcc ggc cag tcg gtt gaa cgt acc gcg cag cag      576
198 Ser Asp Leu Tyr Arg Ala Gly Gln Ser Val Glu Arg Thr Ala Gln Gln
199          180          185          190
201 gca gcc gca ttc gta aaa gcg tat cga gag gca gtg aaa tga      618
202 Ala Ala Ala Phe Val Lys Ala Tyr Arg Glu Ala Val Lys
203          195          200          205
206 <210> SEQ ID NO: 4
207 <211> LENGTH: 205
208 <212> TYPE: PRT
209 <213> ORGANISM: Klebsiella pneumoniae

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211 <400> SEQUENCE: 4

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213 Met Gln Trp Gln Thr Asn Leu Pro Leu Ile Ala Ile Leu Arg Gly Ile
214 1 5 10 15
217 Thr Pro Asp Glu Ala Leu Ala His Val Gly Ala Val Ile Asp Ala Gly
218 20 25 30
221 Phe Asp Ala Val Glu Ile Pro Leu Asn Ser Pro Gln Trp Glu Lys Ser
222 35 40 45
225 Ile Pro Gln Val Val Asp Ala Tyr Gly Glu Gln Ala Leu Ile Gly Ala
226 50 55 60
229 Gly Thr Val Leu Gln Pro Glu Gln Val Asp Arg Leu Ala Ala Met Gly
230 65 70 75 80
233 Cys Arg Leu Ile Val Thr Pro Asn Ile Gln Pro Glu Val Ile Arg Arg
234 85 90 95
237 Ala Val Gly Tyr Gly Met Thr Val Cys Pro Gly Cys Ala Thr Ala Ser
238 100 105 110
241 Glu Ala Phe Ser Ala Leu Asp Ala Gly Ala Gln Ala Leu Lys Ile Phe
242 115 120 125
245 Pro Ser Ser Ala Phe Gly Pro Asp Tyr Ile Lys Ala Leu Lys Ala Val
246 130 135 140
249 Leu Pro Pro Glu Val Pro Val Phe Ala Val Gly Gly Val Thr Pro Glu
250 145 150 155 160
253 Asn Leu Ala Gln Trp Ile Asn Ala Gly Cys Val Gly Ala Gly Leu Gly
254 165 170 175
257 Ser Asp Leu Tyr Arg Ala Gly Gln Ser Val Glu Arg Thr Ala Gln Gln
258 180 185 190
261 Ala Ala Ala Phe Val Lys Ala Tyr Arg Glu Ala Val Lys
262 195 200 205

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265 <210> SEQ ID NO: 5

266 <211> LENGTH: 618

267 <212> TYPE: DNA

268 <213> ORGANISM: Salmonella typhimurium

271 <220> FEATURE:

272 <221> NAME/KEY: CDS

273 <222> LOCATION: (1)..(615)

274 <223> OTHER INFORMATION: dgoA CDS for KDPGal Aldolase

276 <400> SEQUENCE: 5

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279 1 5 10 15
281 acg ccc gat gat gcc ctg gcg cac gtt ggc gcg gtg gtg gat gcg gga 96
282 Thr Pro Asp Asp Ala Leu Ala His Val Gly Ala Val Val Asp Ala Gly
283 20 25 30
285 ttt gac gct ata gaa att ccg ctt aac tcc cca cag tgg gaa aaa agc 144
286 Phe Asp Ala Ile Glu Ile Pro Leu Asn Ser Pro Gln Trp Glu Lys Ser
287 35 40 45
289 att tct tcc gtg gtg aag gcg tat ggc ggc agg gcg ctt att ggc gct 192
290 Ile Ser Ser Val Val Lys Ala Tyr Gly Gly Arg Ala Leu Ile Gly Ala
291 50 55 60
293 ggt acc gta ctg aaa ccg gaa cag gta gac cag ctt gcc ggg atg ggc 240

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294 Gly Thr Val Leu Lys Pro Glu Gln Val Asp Gln Leu Ala Gly Met Gly
295 65 70 75 80
297 tgc aag ctg atc gtc acg ccg aat atc caa ccg gag gtg atc cgc cgg 288
298 Cys Lys Leu Ile Val Thr Pro Asn Ile Gln Pro Glu Val Ile Arg Arg
299 85 90 95
301 gcg gtg agc tat ggc atg acc gtg tgt ccg ggc tgc gcc acg gca acg 336
302 Ala Val Ser Tyr Gly Met Thr Val Cys Pro Gly Cys Ala Thr Ala Thr
303 100 105 110
305 gaa gcc ttt tct gcg ctg gat gca ggc gca cag gcg tta aaa att ttc 384
306 Glu Ala Phe Ser Ala Leu Asp Ala Gly Ala Gln Ala Leu Lys Ile Phe
307 115 120 125
309 ccg tcg tcg gcg ttt ggt ccg ggc tac atc agc gcg ctg aaa gcg gta 432
310 Pro Ser Ser Ala Phe Gly Pro Gly Tyr Ile Ser Ala Leu Lys Ala Val
311 130 135 140
313 ctt ccg ccg gat gtt ccg cta ttt gcc gtc ggc ggc gtg acg ccg gaa 480
314 Leu Pro Pro Asp Val Pro Leu Phe Ala Val Gly Gly Val Thr Pro Glu
315 145 150 155 160
317 aac cta gcg caa tgg att aaa gca ggc tgt gtg ggc gcg gga ttg ggt 528
318 Asn Leu Ala Gln Trp Ile Lys Ala Gly Cys Val Gly Ala Gly Leu Gly
319 165 170 175
321 agc gat ctc tat cgc gcc ggg caa tcc gtt gaa cgc acc gcg cag cag 576
322 Ser Asp Leu Tyr Arg Ala Gly Gln Ser Val Glu Arg Thr Ala Gln Gln
323 180 185 190
325 gct gcg gca ttt gtt aat gcg tat cga gag gca gtg aaa tga 618
326 Ala Ala Ala Phe Val Asn Ala Tyr Arg Glu Ala Val Lys
327 195 200 205
330 <210> SEQ ID NO: 6
331 <211> LENGTH: 205
332 <212> TYPE: PRT
333 <213> ORGANISM: Salmonella typhimurium
335 <400> SEQUENCE: 6
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338 1 5 10 15
341 Thr Pro Asp Asp Ala Leu Ala His Val Gly Ala Val Val Asp Ala Gly
342 20 25 30
345 Phe Asp Ala Ile Glu Ile Pro Leu Asn Ser Pro Gln Trp Glu Lys Ser
346 35 40 45
349 Ile Ser Ser Val Val Lys Ala Tyr Gly Gly Arg Ala Leu Ile Gly Ala
350 50 55 60
353 Gly Thr Val Leu Lys Pro Glu Gln Val Asp Gln Leu Ala Gly Met Gly
354 65 70 75 80
357 Cys Lys Leu Ile Val Thr Pro Asn Ile Gln Pro Glu Val Ile Arg Arg
358 85 90 95
361 Ala Val Ser Tyr Gly Met Thr Val Cys Pro Gly Cys Ala Thr Ala Thr
362 100 105 110
365 Glu Ala Phe Ser Ala Leu Asp Ala Gly Ala Gln Ala Leu Lys Ile Phe
366 115 120 125
369 Pro Ser Ser Ala Phe Gly Pro Gly Tyr Ile Ser Ala Leu Lys Ala Val
370 130 135 140

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 04/10/2006
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34

VERIFICATION SUMMARY

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Input Set : F:\6550-086POA SeqListing.ST25.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date